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RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/836,470

DATE: 11/20/2001  
 TIME: 19:11:34

Input Set : A:\836470.txt  
 Output Set: N:\CRF3\11202001\I836470.raw

**ENTERED**

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:  
 5 (i) APPLICANT: Witte, Owen N.  
 6 Weng, Zhigang  
 8 (ii) TITLE OF INVENTION: IDENTIFICATION OF A G PROTEIN-COUPLED  
 9 RECEPTOR TRANSCRIPTIONALLY REGULATED BY PROTEIN  
 10 TYROSINE KINASE SIGNALING IN HEMATOPOIETIC CELLS  
 12 (iii) NUMBER OF SEQUENCES: 40  
 14 (iv) CORRESPONDENCE ADDRESS:  
 15 (A) ADDRESSEE: Knobbe, Martens, Olson & Bear  
 16 (B) STREET: 620 Newport Center Drive, 16th Floor  
 17 (C) CITY: Newport Beach  
 18 (D) STATE: CA  
 19 (E) COUNTRY: U.S.A.  
 20 (F) ZIP: 92660  
 22 (v) COMPUTER READABLE FORM:  
 23 (A) MEDIUM TYPE: Diskette  
 24 (B) COMPUTER: IBM Compatible  
 25 (C) OPERATING SYSTEM: DOS  
 26 (D) SOFTWARE: FastSEQ for Windows Version 2.0  
 28 (vi) CURRENT APPLICATION DATA:  
 C--> 29 (A) APPLICATION NUMBER: US/09/836,470  
 C--> 30 (B) FILING DATE: 18-Apr-2001  
 31 (C) CLASSIFICATION:  
 33 (vii) PRIOR APPLICATION DATA:  
 34 (A) APPLICATION NUMBER: US/08/969,815  
 35 (B) FILING DATE:  
 37 (viii) ATTORNEY/AGENT INFORMATION:  
 38 (A) NAME: Bartfeld, Neil S  
 39 (B) REGISTRATION NUMBER: 39,901  
 40 (C) REFERENCE/DOCKET NUMBER: UCLA015.001A  
 42 (ix) TELECOMMUNICATION INFORMATION:  
 43 (A) TELEPHONE: 619-235-8550  
 44 (B) TELEFAX: 619-235-0176  
 45 (C) TELEX:  
 48 (2) INFORMATION FOR SEQ ID NO: 1:  
 50 (i) SEQUENCE CHARACTERISTICS:  
 51 (A) LENGTH: 1507 base pairs  
 52 (B) TYPE: nucleic acid  
 53 (C) STRANDEDNESS: single  
 54 (D) TOPOLOGY: linear  
 56 (ii) MOLECULE TYPE: cDNA  
 57 (ix) FEATURE:  
 59 (A) NAME/KEY: Coding Sequence  
 60 (B) LOCATION: 147...1292  
 61 (D) OTHER INFORMATION:  
 63 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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65	AAACCTCCCA	GCTGGGCCTG	CAGAGGGGTG	CTCAGCCCTG	CCTCAGGACG	GGCCTGCCCT	60
66	GTGCTGCCTC	AGGACTGGCT	TGGGTCATTT	TAAGCTGCCA	GAGCCACCTT	CACAAGGGGG	120
67	TCCACAGAAC	TCACATAGGA	GCCACC	ATG	AGA	TCA GAA CCT ACC AAT GCA GCA	173
68				Met	Arg	Ser Glu Pro Thr Asn Ala Ala	
69				1		5	
71	GGA AAC ACC ACA	CTG GGG GTT ACC	TCC GTT CTT	CAG AGC ACC	TCA GTA		221
72	Gly Asn Thr Thr	Leu Gly Val Thr	Ser Val Leu	Gln Ser Thr	Ser Val		
73	10	15	20	25			
75	CCT TCT TCT	GAG ACC TGC CAC	GTC TCC TAC	GAG GAG AGC	AGA GTG GTC		269
76	Pro Ser Ser	Glu Thr Cys His	Val Ser Tyr	Glu Glu Ser	Arg Val Val		
77		30	35	40			
79	CTG GTG GTG	GTG TAC AGT GCC	GTG TGC CTG	CTG GGC CTA	CCA GCC AAC		317
80	Leu Val Val	Val Tyr Ser Ala	Val Cys Leu	Leu Gly Leu	Pro Ala Asn		
81		45	50	55			
83	TGC CTG ACT	GCC TGG CTG	ACG CTG CTG	CAA GTC CTG	CAG AGG AAC	GTG	365
84	Cys Leu Thr	Ala Trp Leu	Thr Leu Leu	Gln Val Leu	Gln Arg Asn	Val	
85		60	65	70			
87	CTA GCC GTC	TAC CTG TTC	TGC CTG TCC	CTC TGT GAG	CTG CTC TAC	ATC	413
88	Leu Ala Val	Tyr Leu Phe	Cys Leu Ser	Leu Cys Glu	Leu Leu Tyr	Ile	
89		75	80	85			
91	AGC ACG GTG	CCA TTG TGG	ATC ATC TAC	ATC CAG AAT	CAG CAC AAA	TGG	461
92	Ser Thr Val	Pro Leu Trp	Ile Ile Tyr	Ile Gln Asn	Gln His Lys	Trp	
93		95	100	105			
95	AAC CTG GGT	CCG CAG GCC	TGC AAG GTG	ACT GCT TAC	ATC TTC TTC	TGC	509
96	Asn Leu Gly	Pro Gln Ala	Cys Lys Val	Thr Ala Tyr	Ile Phe Phe	Cys	
97		110	115	120			
99	AAC ATC TAC	ATC AGC ATC	CTC TTG CTC	TGC TGC ATT	TCC TGC GAC	CGC	557
100	Asn Ile Tyr	Ile Ser Ile	Leu Leu Leu	Cys Cys Ile	Ser Cys Asp	Arg	
101		125	130	135			
103	TAC ATG GCC	GTG GTC TAT	GCA CTG GAG	AGC CGA GGC	CAC CGC CAC	CAG	605
104	Tyr Met Ala	Val Val Tyr	Ala Leu Glu	Ser Arg Gly	His Arg His	Gln	
105		140	145	150			
107	AGG ACT GCT	GTC ACC ATT	TCT GCG TGT	GTG ATT CTT	CTT GTT GGA	CTT	653
108	Arg Thr Ala	Val Thr Ile	Ser Ala Cys	Val Ile Leu	Leu Val Gly	Leu	
109		155	160	165			
111	GTT AAC TAT	CCA GTG TTT	GAC ATG AAG	GTG GAG AAG	AGT TTC TGC	TTT	701
112	Val Asn Tyr	Pro Val Phe	Asp Met Lys	Val Glu Lys	Ser Phe Cys	Phe	
113		170	175	180			
115	GAG CCC CTG	AGG ATG AAC	AGC AAG ATA	GCC GGC TAC	CAC TAC CTG	CGT	749
116	Glu Pro Leu	Arg Met Asn	Ser Lys Ile	Ala Gly Tyr	His Tyr Leu	Arg	
117		190	195	200			
119	TTC ACC TTT	GGC TTT GCC	ATC CCT CTC	GGC ATC CTG	GCG TTC ACC	AAT	797
120	Phe Thr Phe	Gly Phe Ala	Ile Pro Leu	Gly Ile Leu	Ala Phe Thr	Asn	
121		205	210	215			
123	CAC CAG ATC	TTC CGG AGC	ATC AAA CTC	AGT GAC AGC	CTG AGC GCT	GCG	845
124	His Gln Ile	Phe Arg Ser	Ile Lys Leu	Ser Asp Ser	Leu Ser Ala	Ala	
125		220	225	230			
127	CAG AAG AAC	AAG GTG AAG	CGC TCC GCC	ATC GCG GTC	ACC ATC TTC		893
128	Gln Lys Asn	Lys Val Lys	Arg Ser Ala	Ile Ala Val	Val Thr Ile	Phe	

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```

129      235      240      245
131 CTG GTC TGC TTT GCT CCC TAC CAC GTG GTA CTC CTC GTC AAA GCT GCC      941
132 Leu Val Cys Phe Ala Pro Tyr His Val Val Leu Leu Val Lys Ala Ala
133 250      255      260      265
135 AGC TTT TCC TTC TAC CAA GGA GAC ATG GAT GCC GTG TGT GCC TTT GAA      989
136 Ser Phe Ser Phe Tyr Gln Gly Asp Met Asp Ala Val Cys Ala Phe Glu
137      270      275      280
139 AGC AGA CTG TAC ACA GTC TCT ATG GTG TTT CTG TGC CTG TCT ACA GTC      1037
140 Ser Arg Leu Tyr Thr Val Ser Met Val Phe Leu Cys Leu Ser Thr Val
141      285      290      295
143 AAC AGT GTG GCT GAC CCC ATC ATC TAC GTG CTG GGT ACA GAC CAC TCT      1085
144 Asn Ser Val Ala Asp Pro Ile Ile Tyr Val Leu Gly Thr Asp His Ser
145      300      305      310
147 CGG CAA GAA GTG TCC AGA ATC CAC ACA GGG TGG AAA AAG TGG TCC ACA      1133
148 Arg Gln Glu Val Ser Arg Ile His Thr Gly Trp Lys Lys Trp Ser Thr
149      315      320      325
151 AAG ACA TAT GTT ACA TGC TCA AAG GAC TCT GAG GAG ACA CAC TTG CCC      1181
152 Lys Thr Tyr Val Thr Cys Ser Lys Asp Ser Glu Glu Thr His Leu Pro
153 330      335      340      345
155 ACA GAG CTT TCA AAC ACA TAC ACC TTC CCC AAT CCC GCG CAC CCT CCA      1229
156 Thr Glu Leu Ser Asn Thr Tyr Thr Phe Pro Asn Pro Ala His Pro Pro
157      350      355      360
159 GGA TCA CAG CCA GCG AAG CTA GGT TTA CTG TGC TCG CCA GAG AGA CTG      1277
160 Gly Ser Gln Pro Ala Lys Leu Gly Leu Leu Cys Ser Pro Glu Arg Leu
161      365      370      375
163 CCT GAG GAG CTC TGC TAAGAGACGA TTGTCCACTC TTCCTCAAAA CTAGCACCAG T      1333
164 Pro Glu Glu Leu Cys
165      380
167 CACACATACC TGGTCCTCTG AGTCACCGTC TGGGGTGTCC ACAGCACTAT AGATGCCTTT      1393
168 GTTCGGGCAC ACGCTGCTGA TCTTTCCTTC CTAAGGCCAC CAACTCTGAA AGTATCTGTT      1453
169 CCTTAAACTG TCCTCAGGCT CCCCTCTATG GAAAGCGGGG CTTGCTAAGG GACC      1507
171 (2) INFORMATION FOR SEQ ID NO: 2:
173 (i) SEQUENCE CHARACTERISTICS:
174 (A) LENGTH: 382 amino acids
175 (B) TYPE: amino acid
176 (C) STRANDEDNESS: single
177 (D) TOPOLOGY: linear
179 (ii) MOLECULE TYPE: protein
180 (v) FRAGMENT TYPE: internal
182 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
184 Met Arg Ser Glu Pro Thr Asn Ala Ala Gly Asn Thr Thr Leu Gly Val
185 1 5 10 15
186 Thr Ser Val Leu Gln Ser Thr Ser Val Pro Ser Ser Glu Thr Cys His
187 20 25 30
188 Val Ser Tyr Glu Glu Ser Arg Val Val Leu Val Val Val Tyr Ser Ala
189 35 40 45
190 Val Cys Leu Leu Gly Leu Pro Ala Asn Cys Leu Thr Ala Trp Leu Thr
191 50 55 60
192 Leu Leu Gln Val Leu Gln Arg Asn Val Leu Ala Val Tyr Leu Phe Cys

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```

193 65          70          75          80
194 Leu Ser Leu Cys Glu Leu Leu Tyr Ile Ser Thr Val Pro Leu Trp Ile
195          85          90          95
196 Ile Tyr Ile Gln Asn Gln His Lys Trp Asn Leu Gly Pro Gln Ala Cys
197          100          105          110
198 Lys Val Thr Ala Tyr Ile Phe Phe Cys Asn Ile Tyr Ile Ser Ile Leu
199          115          120          125
200 Leu Leu Cys Cys Ile Ser Cys Asp Arg Tyr Met Ala Val Val Tyr Ala
201          130          135          140
202 Leu Glu Ser Arg Gly His Arg His Gln Arg Thr Ala Val Thr Ile Ser
203          145          150          155          160
204 Ala Cys Val Ile Leu Leu Val Gly Leu Val Asn Tyr Pro Val Phe Asp
205          165          170          175
206 Met Lys Val Glu Lys Ser Phe Cys Phe Glu Pro Leu Arg Met Asn Ser
207          180          185          190
208 Lys Ile Ala Gly Tyr His Tyr Leu Arg Phe Thr Phe Gly Phe Ala Ile
209          195          200          205
210 Pro Leu Gly Ile Leu Ala Phe Thr Asn His Gln Ile Phe Arg Ser Ile
211          210          215          220
212 Lys Leu Ser Asp Ser Leu Ser Ala Ala Gln Lys Asn Lys Val Lys Arg
213          225          230          235          240
214 Ser Ala Ile Ala Val Val Thr Ile Phe Leu Val Cys Phe Ala Pro Tyr
215          245          250          255
216 His Val Val Leu Leu Val Lys Ala Ala Ser Phe Ser Phe Tyr Gln Gly
217          260          265          270
218 Asp Met Asp Ala Val Cys Ala Phe Glu Ser Arg Leu Tyr Thr Val Ser
219          275          280          285
220 Met Val Phe Leu Cys Leu Ser Thr Val Asn Ser Val Ala Asp Pro Ile
221          290          295          300
222 Ile Tyr Val Leu Gly Thr Asp His Ser Arg Gln Glu Val Ser Arg Ile
223          305          310          315          320
224 His Thr Gly Trp Lys Lys Trp Ser Thr Lys Thr Tyr Val Thr Cys Ser
225          325          330          335
226 Lys Asp Ser Glu Glu Thr His Leu Pro Thr Glu Leu Ser Asn Thr Tyr
227          340          345          350
228 Thr Phe Pro Asn Pro Ala His Pro Pro Gly Ser Gln Pro Ala Lys Leu
229          355          360          365
230 Gly Leu Leu Cys Ser Pro Glu Arg Leu Pro Glu Glu Leu Cys
231          370          375          380

```

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2938 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 901...2040

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246 (D) OTHER INFORMATION:

248 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

250	GGGAGGGGTG	CNANGCTAGC	CACGCAGGCG	GGGCCCTGGG	TCATTTTAAN	CTCTCAGAGT	60
251	GAACGTCTTG	ATAGGACCGA	CAANACNCAT	NACNTGTACT	TAGATAGCTT	ATCTTANANC	120
252	CACNCTGANA	TTGGAACCCG	CAAAATATGC	CNGGGAGGAA	GGTGAGCAAG	GGACACGACA	180
253	CTCACCCGGA	TAAACCCAAC	AAGCGCAGCG	AGGCTGTGGG	GAAACCGGAN	CCCTGCACAC	240
254	CGCCGGGGGA	AGGTGGGCCN	CCGCCACCAC	CGTGGAAGAA	CAGCGCGGAN	GCACCCACG	300
255	AGATGAGACG	GAAGTCCCGT	GAGATCCAGC	AATNCCNACT	GTGGGTCTGA	CCCAGGATAN	360
256	CGGAAAGCAG	GGACGTGAAC	AGCCCTCCTC	ATGTTCTTGA	CACCGTCATT	CTCAGCAGCT	420
257	CAGCTAAGGC	ACAGAGGCAG	CCGAGCGTCT	GTCAGCAGAG	TCGTGGCTGA	GCAGAACACG	480
258	CCACACGCCA	CACGCCACAC	GCCACACGTG	CAGGATTGCT	CAAGATGGAA	GGGCACAGTG	540
259	GAATATATAT	ATATATTTAT	ATTTTGGCG	AGACCCTGGA	GGACACACTG	AATACAATGG	600
260	AATACCATCC	CGCCTTTGAA	AGGAAGGGAA	ATCCTGGCAC	ACGCTGCAAC	AGGAGGGAGC	660
261	TTGAGGACAC	TGTGGTGAGT	GGAGCACGTG	AGACACGGAA	GGACACACGC	TGAAGACACG	720
262	CAGAGATGCC	CACCCACGTG	GGGAGGTGAC	AGGGGAGCCC	AGCGCACAGA	GACAAAGTGG	780
263	AATGGAGGCC	TGGGGGCTGG	GAGCAAATGC	GGAGCGAGTG	CTTCCTGGGG	CAGAGTCTCC	840
264	GTTTGGGAAG	ATGAGAAGGT	TCTGCCGACG	GATGCTGGCG	ATGGTTGCAG	AAGAATGTGA	900
265	ATG TGC CCA	ATG CTA CTG	AAA AAC	GGT TAC AAT	GGA AAC GCC	ACC CCA	948
266	Met Cys Pro	Met Leu Leu	Lys Asn Gly	Tyr Asn Gly	Asn Ala Thr	Pro	
267	1	5	10	15			
269	GTG ACC ACC	ACT GCC CCG	TGG GCC TCC	CTG GGC CTC	TCC GCC AAG	ACC	996
270	Val Thr Thr	Thr Ala Pro	Trp Ala Ser	Leu Gly Leu	Ser Ala Lys	Thr	
271		20	25	30			
273	TGC AAC AAC	GTG TCC TTC	GAA GAG AGC	AGG ATA GTC	CTG GTC GTG	GTG	1044
274	Cys Asn Asn	Val Ser Phe	Glu Glu Ser	Arg Ile Val	Leu Val Val	Val	
275		35	40	45			
277	TAC AGC GCG	GTG TGC ACG	CTG GGG GTG	CCG GCC AAC	TGC CTG ACT	GCG	1092
278	Tyr Ser Ala	Val Cys Thr	Leu Gly Val	Pro Ala Asn	Cys Leu Thr	Ala	
279		50	55	60			
281	TGG CTG GCG	CTG CTG CAG	GTA CTG CAG	GGC AAC GTG	CTG GCC GTC	TAC	1140
282	Trp Leu Ala	Leu Leu Gln	Val Leu Gln	Gly Asn Val	Leu Ala Val	Tyr	
283		65	70	75		80	
285	CTG CTC TGC	CTG GCA CTC	TGC GAG CTG	CTG TAC ACA	GGC ACG CTG	CCA	1188
286	Leu Leu Cys	Leu Ala Leu	Cys Glu Leu	Leu Tyr Thr	Gly Thr Leu	Pro	
287		85	90	95			
289	CTC TGG GTC	ATC TAT ATC	CGC AAC CAG	CAC CGC TGG	ACC CTA GGC	CTG	1236
290	Leu Trp Val	Ile Tyr Ile	Arg Asn Gln	His Arg Trp	Thr Leu Gly	Leu	
291		100	105	110			
293	CTG GCC TGC	AAG GTG ACC	GCC TAC ATC	TTC TTC TGC	AAC ATC TAC	GTC	1284
294	Leu Ala Cys	Lys Val Thr	Ala Tyr Ile	Phe Phe Cys	Asn Ile Tyr	Val	
295		115	120	125			
297	AGC ATC CTC	TTC CTG TGC	TGC ATC TCC	TGC GAC CGC	TTC GTG GCC	GTG	1332
298	Ser Ile Leu	Phe Leu Cys	Cys Ile Ser	Cys Asp Arg	Phe Val Ala	Val	
299		130	135	140			
301	GTG TAC GCG	CTG GAG AGT	CGG GGC CGC	CGC CGG AGG	ACC GCC ATC		1380
302	Val Tyr Ala	Leu Glu Ser	Arg Gly Arg	Arg Arg Arg	Arg Thr Ala	Ile	
303		145	150	155		160	
305	CTC ATC TCC	GCC TGC ATC	TTC ATC CTC	GTC GGG ATC	GTT CAC TAC	CCG	1428
306	Leu Ile Ser	Ala Cys Ile	Phe Ile Leu	Val Gly Ile	Val His Tyr	Pro	

## VERIFICATION SUMMARY

DATE: 11/20/2001

PATENT APPLICATION: US/09/836,470

TIME: 19:11:35

Input Set : A:\836470.txt

Output Set: N:\CRF3\11202001\I836470.raw

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]